SEQUENCE LISTING

<110> Alnemri, Emad S.

<120> NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND
      METHODS OF USE THEREOF

<130> 480140.432D3

<140> US
<141> 2002-02-12

<160> 6

<170> PatentIn Ver. 2.0

<210> 1
<211> 1236
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1233)

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atg gaa caa cgg gga cag aac gcc ccg gcc gct tcg ggg gcc cgg aaa      48
Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
1               5                   10                  15

agg cac ggc cca gga ccc agg gag gcg cgg gga gcc agg cct ggg ctc      96
Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Leu
                20                  25                  30

cgg gtc ccc aag acc ctt gtg ctc gtt gtc gcc gcg gtc ctg ctg ttg     144
Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
            35                  40                  45

gtc tca gct gag tct gct ctg atc acc caa caa gac cta gct ccc cag     192
Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
        50                  55                  60

cag aga gtg gcc cca caa caa aag agg tcc agc ccc tca gag gga ttg     240
Gln Arg Val Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
65                  70                  75                  80

tgt cca cct gga cac cat atc tca gaa gac ggt aga gat tgc atc tcc     288
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
                85                  90                  95

tgc aaa tat gga cag gac tat agc act cac tgg aat gac ctc ctt ttc     336
Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
                100                 105                 110

tgc ttg cgc tgc acc agg tgt gat tca ggt gaa gtg gag cta agt ccc     384
Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
            115                 120                 125
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tgc acc acg acc aga aac aca gtg tgt cag tgc gaa gaa ggc acc ttc      432
Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
130             135             140

cgg gaa gaa gat tct cct gag atg tgc cgg aag tgc cgc aca ggg tgt      480
Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
145             150             155             160

ccc aga ggg atg gtc aag gtc ggt gat tgt aca ccc tgg agt gac atc      528
Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
                165             170             175

gaa tgt gtc cac aaa gaa tca ggc atc atc ata gga gtc aca gtt gca      576
Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala
                180             185             190

gcc gta gtc ttg att gtg gct gtg ttt gtt tgc aag tct tta ctg tgg      624
Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp
            195             200             205

aag aaa gtc ctt cct tac ctg aaa ggc atc tgc tca ggt ggt ggt ggg      672
Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly
210             215             220

gac cct gag cgt gtg gac aga agc tca caa cga cct ggg gct gag gac      720
Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
225             230             235             240

aat gtc ctc aat gag atc gtg agt atc ttg cag ccc acc cag gtc cct      768
Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
                245             250             255

gag cag gaa atg gaa gtc cag gag cca gca gag cca aca ggt gtc aac      816
Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn
            260             265             270

atg ttg tcc ccc ggg gag tca gag cat ctg ctg gaa ccg gca gaa gct      864
Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
            275             280             285

gaa agg tct cag agg agg agg ctg ctg gtt cca gca aat gaa ggt gat      912
Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp
290             295             300

ccc act gag act ctg aga cag tgc ttc gat gac ttt gca gac ttg gtg      960
Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val
305             310             315             320

ccc ttt gac tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac     1008
Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp
                325             330             335

aat gag ata aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc     1056
Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr
                340             345             350
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ttg tac acg atg ctg ata aag tgg gtc aac aaa acc ggg cga gat gcc   1104
Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala
        355             360             365

tct gtc cac acc ctg ctg gat gcc ttg gag acg ctg gga gag aga ctt   1152
Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu
        370             375             380

gcc aag cag aag att gag gac cac ttg ttg agc tct gga aag ttc atg   1200
Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met
385             390             395             400

tat cta gaa ggt aat gca gac tct gcc atg tcc taa                   1236
Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
            405             410
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<211> 411
<212> PRT
<213> Homo sapiens

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Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
1               5               10              15

Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Leu
            20              25              30

Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
        35              40              45

Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
    50              55              60

Gln Arg Val Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
65              70              75              80

Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
            85              90              95

Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
            100             105             110

Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
        115             120             125

Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
130             135             140

Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
145             150             155             160

Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
            165             170             175

Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala
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                  180                    185                    190

Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp
        195                    200                    205

Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly
        210                    215                    220

Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
225                    230                    235                    240

Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
                245                    250                    255

Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn
                260                    265                    270

Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
        275                    280                    285

Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp
        290                    295                    300

Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val
305                    310                    315                    320

Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp
                325                    330                    335

Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr
                340                    345                    350

Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala
        355                    360                    365

Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu
        370                    375                    380

Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met
385                    390                    395                    400

Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
                405                    410
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(897)

<400> 3
atg caa ggg gtg aag gag cgc ttc cta ccg tta ggg aac tct ggg gac    48
Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp
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         1                   5                  10                  15

aga  gcg  ccc  cgg  ccg  cct  gat  ggc  cga  ggc  agg  gtg  cga  ccc  agg  acc    96
Arg  Ala  Pro  Arg  Pro  Pro  Asp  Gly  Arg  Gly  Arg  Val  Arg  Pro  Arg  Thr
               20                       25                       30

caa  gac  ggc  gtc  ggg  aac  cat  acc  atg  gcc  cgg  atc  ccc  aag  acc  cta    144
Gln  Asp  Gly  Val  Gly  Asn  His  Thr  Met  Ala  Arg  Ile  Pro  Lys  Thr  Leu
               35                       40                       45

aag  ttc  gtc  gtc  gtc  atc  gtc  gcg  gtc  ctg  ctg  cca  gtc  cta  gct  tac    192
Lys  Phe  Val  Val  Val  Ile  Val  Ala  Val  Leu  Leu  Pro  Val  Leu  Ala  Tyr
          50                       55                       60

tct  gcc  acc  act  gcc  cgg  cag  gag  gaa  gtt  ccc  cag  cag  aca  gtg  gcc    240
Ser  Ala  Thr  Thr  Ala  Arg  Gln  Glu  Glu  Val  Pro  Gln  Gln  Thr  Val  Ala
65                       70                       75                       80

cca  cag  caa  cag  agg  cac  agc  ttc  aag  ggg  gag  gag  tgt  cca  gca  gga    288
Pro  Gln  Gln  Gln  Arg  His  Ser  Phe  Lys  Gly  Glu  Glu  Cys  Pro  Ala  Gly
                    85                       90                       95

tct  cat  aga  tca  gaa  cat  act  gga  gcc  tgt  aac  ccg  tgc  aca  gag  ggt    336
Ser  His  Arg  Ser  Glu  His  Thr  Gly  Ala  Cys  Asn  Pro  Cys  Thr  Glu  Gly
               100                      105                      110

gtg  gat  tac  acc  aac  gct  tcc  aac  aat  gaa  cct  tct  tgc  ttc  cca  tgt    384
Val  Asp  Tyr  Thr  Asn  Ala  Ser  Asn  Asn  Glu  Pro  Ser  Cys  Phe  Pro  Cys
          115                      120                      125

aca  gtt  tgt  aaa  tca  gat  caa  aaa  cat  aaa  agt  tcc  tgc  acc  atg  acc    432
Thr  Val  Cys  Lys  Ser  Asp  Gln  Lys  His  Lys  Ser  Ser  Cys  Thr  Met  Thr
          130                      135                      140

aga  gac  aca  gtg  tgt  cag  tgt  aaa  gaa  ggc  acc  ttc  cgg  aat  gaa  aac    480
Arg  Asp  Thr  Val  Cys  Gln  Cys  Lys  Glu  Gly  Thr  Phe  Arg  Asn  Glu  Asn
145                      150                      155                      160

tcc  cca  gag  atg  tgc  cgg  aag  tgt  agc  agg  tgc  cct  agt  ggg  gaa  gtc    528
Ser  Pro  Glu  Met  Cys  Arg  Lys  Cys  Ser  Arg  Cys  Pro  Ser  Gly  Glu  Val
               165                      170                      175

caa  gtc  agt  aat  tgt  acg  tcc  tgg  gat  gat  atc  cag  tgt  gtt  gaa  gaa    576
Gln  Val  Ser  Asn  Cys  Thr  Ser  Trp  Asp  Asp  Ile  Gln  Cys  Val  Glu  Glu
               180                      185                      190

ttt  ggt  gcc  aat  gcc  act  gtg  gaa  acc  cca  gct  gct  gaa  gag  aca  atg    624
Phe  Gly  Ala  Asn  Ala  Thr  Val  Glu  Thr  Pro  Ala  Ala  Glu  Glu  Thr  Met
               195                      200                      205

aac  acc  agc  ccg  ggg  act  cct  gcc  cca  gct  gct  gaa  gag  aca  atg  aac    672
Asn  Thr  Ser  Pro  Gly  Thr  Pro  Ala  Pro  Ala  Ala  Glu  Glu  Thr  Met  Asn
     210                      215                      220

acc  agc  cca  ggg  act  cct  gcc  cca  gct  gct  gaa  gag  aca  atg  acc  acc    720
Thr  Ser  Pro  Gly  Thr  Pro  Ala  Pro  Ala  Ala  Glu  Glu  Thr  Met  Thr  Thr
225                      230                      235                      240
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agc ccg ggg act cct gcc cca gct gct gaa gag aca atg acc acc agc     768
Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser
                245             250             255

ccg ggg act cct gcc cca gct gct gaa gag aca atg acc acc agc ccg     816
Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser Pro
            260             265             270

ggg act cct gcc tct tct cat tac ctc tca tgc acc atc gta ggg atc     864
Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
        275             280             285

ata gtt cta att gtg ctt ctg att gtg ttt gtt tga                     900
Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
        290             295
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<210> 4
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<212> PRT
<213> Homo sapiens

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Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr
            20              25              30

Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro Lys Thr Leu
        35              40              45

Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro Val Leu Ala Tyr
    50              55              60

Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala
65              70              75              80

Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly
                85              90              95

Ser His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly
            100             105             110

Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys
        115             120             125

Thr Val Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr
    130             135             140

Arg Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn
145             150             155             160

Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu Val
            165             170             175
```

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Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val Glu Glu
            180                 185             190

Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met
            195             200             205

Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Asn
            210             215             220

Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
225             230             235             240

Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser
            245             250             255

Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser Pro
            260             265             270

Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
            275             280             285

Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
            290             295
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<212> DNA
<213> Homo sapiens

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Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
1               5                   10                  15

agg cac ggc cca gga ccc agg gag gcg cgg gga gcc agg cct ggg ctc    96
Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Leu
                20                  25                  30

cgg gtc ccc aag acc ctt gtg ctc gtt gtc gcc gcg gtc ctg ctg ttg   144
Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
            35                  40                  45

gtc tca gct gag tct gct ctg atc acc caa caa gac cta gct ccc cag   192
Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
        50                  55                  60

cag aga gtg gcc cca caa caa aag agg tcc agc ccc tca gag gga ttg   240
Gln Arg Val Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
65                  70                  75                  80

tgt cca cct gga cac cat atc tca gaa gac ggt aga gat tgc atc tcc   288
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
```

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                        85                    90                    95

tgc aaa tat gga cag gac tat agc act cac tgg aat gac ctc ctt ttc    336
Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
            100                 105                 110

tgc ttg cgc tgc acc agg tgt gat tca ggt gaa gtg gag cta agt ccc    384
Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
            115                 120                 125

tgc acc acg acc aga aac aca gtg tgt cag tgc gaa gaa ggc acc ttc    432
Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
130                 135                 140

cgg gaa gaa gat tct cct gag atg tgc cgg aag tgc cgc aca ggg tgt    480
Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
145                 150                 155                 160

ccc aga ggg atg gtc aag gtc ggt gat tgt aca ccc tgg agt gac atc    528
Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
            165                 170                 175

gaa tgt gtc cac aaa gaa tca ggt aca aag cac agt ggg gaa gcc cca    576
Glu Cys Val His Lys Glu Ser Gly Thr Lys His Ser Gly Glu Ala Pro
            180                 185                 190

gct gtg gag gag acg gtg acc tcc agc cca ggg act cct gcc tct ccc    624
Ala Val Glu Glu Thr Val Thr Ser Ser Pro Gly Thr Pro Ala Ser Pro
            195                 200                 205

tgt tct ctc tca ggc atc atc ata gga gtc aca gtt gca gcc gta gtc    672
Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
            210                 215                 220

ttg att gtg gct gtg ttt gtt tgc aag tct tta ctg tgg aag aaa gtc    720
Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys Val
225                 230                 235                 240

ctt cct tac ctg aaa ggc atc tgc tca ggt ggt ggt ggg gac cct gag    768
Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp Pro Glu
                    245                 250                 255

cgt gtg gac aga agc tca caa cga cct ggg gct gag gac aat gtc ctc    816
Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn Val Leu
                260                 265                 270

aat gag atc gtg agt atc ttg cag ccc acc cag gtc cct gag cag gaa    864
Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu Gln Glu
            275                 280                 285

atg gaa gtc cag gag cca gca gag cca aca ggt gtc aac aaa acc ggg    912
Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Lys Thr Gly
            290                 295                 300

cga gat gcc tct gtc cac acc ctg ctg gat gcc ttg gag acg ctg gga    960
Arg Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly
305                 310                 315                 320
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gag aga ctt gcc aag cag aag att gag gac cac ttg ttg agc tct gga     1008
Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly
                325                 330                 335

aag ttc atg tat cta gaa ggt aat gca gac tct gcc atg tcc taa         1053
Lys Phe Met Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
                340                 345                 350


<210> 6
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<212> PRT
<213> Homo sapiens

<400> 6
Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
1               5                   10                  15

Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Leu
                20                  25                  30

Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
                35                  40                  45

Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
        50                  55                  60

Gln Arg Val Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
65                  70                  75                  80

Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
                85                  90                  95

Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
                100                 105                 110

Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
        115                 120                 125

Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
        130                 135                 140

Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
145                 150                 155                 160

Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
                165                 170                 175

Glu Cys Val His Lys Glu Ser Gly Thr Lys His Ser Gly Glu Ala Pro
                180                 185                 190

Ala Val Glu Glu Thr Val Thr Ser Ser Pro Gly Thr Pro Ala Ser Pro
                195                 200                 205

Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
        210                 215                 220
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Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys Val
225   230   235   240

Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp Pro Glu
              245   250   255

Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn Val Leu
              260   265   270

Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu Gln Glu
          275   280   285

Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Lys Thr Gly
      290   295   300

Arg Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly
305   310   315   320

Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly
              325   330   335

Lys Phe Met Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
              340   345   350